

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
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Application Serial Number: 10/554,026  
Source: pg 10  
Date Processed by STIC: 11/1/05

# ***ENTERED***



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## RAW SEQUENCE LISTING

DATE: 11/01/2005

PATENT APPLICATION: US/10/554,026

TIME: 10:53:13

Input Set : A:\Q90951 Sequence Listing.txt

Output Set: N:\CRF4\11012005\J554026.raw

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3 <110> APPLICANT: Japan Science and Technology Agency
W--> 4 <120> TITLE OF INVENTION: APOPTOSIS-INDUCING AGENT AND METHOD FOR INDUCING APOPTOSIS
W--> 5 <130> FILE REFERENCE: Q90951
C--> 6 <140> CURRENT APPLICATION NUMBER: US/10/554,026
C--> 6 <141> CURRENT FILING DATE: 2005-10-21
6 <150> PRIOR APPLICATION NUMBER: JP 2003-116299
7 <151> PRIOR FILING DATE: 2003-04-21
W--> 8 <160> NUMBER OF SEQ ID: 14
10 <170> SOFTWARE: PatentIn version 3.1
12 <210> SEQ ID NO: 1
13 <211> LENGTH: 1853
14 <212> TYPE: DNA
15 <213> ORGANISM: Homo sapiens
17 <220> FEATURE:
18 <221> NAME/KEY: CDS
19 <222> LOCATION: (65)..(1693)
21 <300> PUBLICATION INFORMATION:
22 <301> AUTHORS: Liu, J. et al.
23 <302> TITLE: Defective interplay of activators with TFIH in xeroderma
24 pigmentosum
25 <303> JOURNAL: Cell
26 <304> VOLUME: 104
27 <305> ISSUE: 3
28 <306> PAGES: 353-353
29 <307> DATE: 2001
30 <308> DATABASE ACCESSION NO: GenBank/NM_14281
31 <309> DATABASE ENTRY DATE: 2001-12-26
32 <313> RELEVANT RESIDUES: 1 TO 1853
34 <400> SEQUENCE: 1
35 atcgcgcgag acagcgggaag gagcaagagt gggaggcgcg cgcggaggcc gcgacggacg 60
37 caag atg gcg acg gcg acc ata gct ctc cag gtc aat ggc cag caa gga 109
38 Met Ala Thr Ala Thr Ile Ala Leu Gln Val Asn Gly Gln Gln Gly
39 1 5 10 15
41 ggg ggg tcc gag ccg gcg gcg gcg gcg gca gtg gtg gca gcg gga gac 157
42 Gly Gly Ser Glu Pro Ala Ala Ala Ala Ala Val Val Ala Ala Gly Asp
43 20 25 30
45 aaa tgg aaa cct cca cag ggc aca gac tcc atc aag atg gag aac ggg 205
46 Lys Trp Lys Pro Pro Gln Gly Thr Asp Ser Ile Lys Met Glu Asn Gly
47 35 40 45
49 cag agc aca gcc gcc aag ctg ggg ctg cct ccc ctg acg ccc gag cag 253
50 Gln Ser Thr Ala Ala Lys Leu Gly Leu Pro Pro Leu Thr Pro Glu Gln
51 50 55 60
53 cag gag gcc ctt cag aag gcc aag aag tac gcc atg gag cag agc atc 301

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54 Gln Glu Ala Leu Gln Lys Ala Lys Lys Tyr Ala Met Glu Gln Ser Ile
55      65      70      75
57 aag agt gtg ctg gtg aag cag acc atc gcg cac cag cag cag cag ctc 349
58 Lys Ser Val Leu Val Lys Gln Thr Ile Ala His Gln Gln Gln Gln Leu
59 80      85      90      95
61 acc aac ctg cag atg gcg gct cag cgg cag cgg gcg ctg gcc atc atg 397
62 Thr Asn Leu Gln Met Ala Ala Gln Arg Gln Arg Ala Leu Ala Ile Met
63      100      105      110
65 tgc cgc gtc tac gtg ggc tct atc tac tat gag ctg ggg gag gac acc 445
66 Cys Arg Val Tyr Val Gly Ser Ile Tyr Tyr Glu Leu Gly Glu Asp Thr
67      115      120      125
69 atc cgc cag gcc ttt gcc ccc ttt ggc ccc atc aag agc atc gac atg 493
70 Ile Arg Gln Ala Phe Ala Pro Phe Gly Pro Ile Lys Ser Ile Asp Met
71      130      135      140
73 tcc tgg gac tcc gtc acc atg aag cac aag ggc ttt gcc ttc gtg gag 541
74 Ser Trp Asp Ser Val Thr Met Lys His Lys Gly Phe Ala Phe Val Glu
75      145      150      155
77 tat gag gtc ccc gaa gct gca cag ctg gcc ttg gag cag atg aac tcg 589
78 Tyr Glu Val Pro Glu Ala Ala Gln Leu Ala Leu Glu Gln Met Asn Ser
79 160      165      170      175
81 gtg atg ctg ggg ggc agg aac atc aag gtg ggc aga ccc agc aac ata 637
82 Val Met Leu Gly Gly Arg Asn Ile Lys Val Gly Arg Pro Ser Asn Ile
83      180      185      190
85 ggg cag gcc cag ccc atc ata gac cag ttg gct gag gag gca cgg gcc 685
86 Gly Gln Ala Gln Pro Ile Ile Asp Gln Leu Ala Glu Glu Ala Arg Ala
87      195      200      205
89 ttc aac cgc atc tac gtg gcc tct gtg cac cag gac ctc tca gac gat 733
90 Phe Asn Arg Ile Tyr Val Ala Ser Val His Gln Asp Leu Ser Asp Asp
91      210      215      220
93 gac atc aag agc gtg ttt gag gcc ttt ggc aag atc aag tcc tgc aca 781
94 Asp Ile Lys Ser Val Phe Glu Ala Phe Gly Lys Ile Lys Ser Cys Thr
95      225      230      235
97 ctg gcc cgg gac ccc aca act ggc aag cac aag ggc tac ggc ttc att 829
98 Leu Ala Arg Asp Pro Thr Thr Gly Lys His Lys Gly Tyr Gly Phe Ile
99 240      245      250      255
101 gag tac gag aag gcc cag tcg tcc caa gat gct gtg tct tcc atg aac 877
102 Glu Tyr Glu Lys Ala Gln Ser Ser Gln Asp Ala Val Ser Ser Met Asn
103      260      265      270
105 ctc ttt gac ctg ggt ggc cag tac ttg cgg gtg ggc aag gct gtc aca 925
106 Leu Phe Asp Leu Gly Gly Gln Tyr Leu Arg Val Gly Lys Ala Val Thr
107      275      280      285
109 ccg ccc atg ccc cta ctc aca cca gcc acg cct gga ggc ctc cca cct 973
110 Pro Pro Met Pro Leu Leu Thr Pro Ala Thr Pro Gly Gly Leu Pro Pro
111      290      295      300
113 gcc gct gct gtg gca gct gct gca gcc act gcc aag atc aca gct cag 1021
114 Ala Ala Ala Val Ala Ala Ala Ala Ala Thr Ala Lys Ile Thr Ala Gln
115      305      310      315
117 gaa gca gtg gcc gga gca gcg gtg ctg ggt acc ctg ggc aca cct gga 1069
118 Glu Ala Val Ala Gly Ala Ala Val Leu Gly Thr Leu Gly Thr Pro Gly

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119 320          325          330          335
121 ctg gtg tcc cca gca ctg acc ctg gcc cag ccc ctg ggc act ttg ccc 1117
122 Leu Val Ser Pro Ala Leu Thr Leu Ala Gln Pro Leu Gly Thr Leu Pro
123          340          345          350
125 cag gct gtc atg gct gcc cag gca cct gga gtc atc aca ggt gtg acc 1165
126 Gln Ala Val Met Ala Ala Gln Ala Pro Gly Val Ile Thr Gly Val Thr
127          355          360          365
129 cca gcc cgt cct cct atc ccg gtc acc atc ccc tcg gtg gga gtg gtg 1213
130 Pro Ala Arg Pro Pro Ile Pro Val Thr Ile Pro Ser Val Gly Val Val
131          370          375          380
133 aac ccc atc ctg gcc agc cct cca acg ctg ggt ctc ctg gag ccc aag 1261
134 Asn Pro Ile Leu Ala Ser Pro Pro Thr Leu Gly Leu Leu Glu Pro Lys
135          385          390          395
137 aag gag aag gaa gaa gag gag ctg ttt ccc gag tca gag cgg cca gag 1309
138 Lys Glu Lys Glu Glu Glu Glu Leu Phe Pro Glu Ser Glu Arg Pro Glu
139 400          405          410          415
141 atg ctg agc gag cag gag cac atg agc atc tcg ggc agt agc gcc cga 1357
142 Met Leu Ser Glu Gln Glu His Met Ser Ile Ser Gly Ser Ser Ala Arg
143          420          425          430
145 cac atg gtg atg cag aag ctg ctc cgc aag cag gag tct aca gtg atg 1405
146 His Met Val Met Gln Lys Leu Leu Arg Lys Gln Glu Ser Thr Val Met
147          435          440          445
149 gtt ctg cgc aac atg gtg gac ccc aag gac atc gat gat gac ctg gaa 1453
150 Val Leu Arg Asn Met Val Asp Pro Lys Asp Ile Asp Asp Asp Leu Glu
151          450          455          460
153 ggg gag gtg aca gag gag tgt ggc aag ttc ggg gcc gtg aac cgc gtc 1501
154 Gly Glu Val Thr Glu Glu Cys Gly Lys Phe Gly Ala Val Asn Arg Val
155          465          470          475
157 atc atc tac caa gag aaa caa ggc gag gag gag gat gca gaa atc att 1549
158 Ile Ile Tyr Gln Glu Lys Gln Gly Glu Glu Glu Asp Ala Glu Ile Ile
159 480          485          490          495
161 gtc aag atc ttt gtg gag ttt tcc ata gcc tct gag act cat aag gcc 1597
162 Val Lys Ile Phe Val Glu Phe Ser Ile Ala Ser Glu Thr His Lys Ala
163          500          505          510
165 atc cag gcc ctc aat ggc cgc tgg ttt gct ggc cgc aag gtg gtg gct 1645
166 Ile Gln Ala Leu Asn Gly Arg Trp Phe Ala Gly Arg Lys Val Val Ala
167          515          520          525
169 gaa gtg tac gac cag gag cgt ttt gat aac agt gac ctc tct gcg tga 1693
170 Glu Val Tyr Asp Gln Glu Arg Phe Asp Asn Ser Asp Leu Ser Ala
171          530          535          540
173 cagtgggtccc tctccccgga cttgcacttg ttccttggtt cctctggggt ttatagtgat 1753
175 acagtgggtgt ccccggggcc aggcgcgctc tgcccagccc agcctacagt gcggataaag 1813
177 gtgcggatgc tgctggccct gaaaaaaaaa aaaaaaaaaa 1853
180 <210> SEQ ID NO: 2
181 <211> LENGTH: 542
182 <212> TYPE: PRT
183 <213> ORGANISM: Homo sapiens
185 <400> SEQUENCE: 2
186 Met Ala Thr Ala Thr Ile Ala Leu Gln Val Asn Gly Gln Gln Gly Gly

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187      1              5              10              15
188 Gly Ser Glu Pro Ala Ala Ala Ala Val Val Ala Ala Gly Asp Lys
189              20              25              30
190 Trp Lys Pro Pro Gln Gly Thr Asp Ser Ile Lys Met Glu Asn Gly Gln
191              35              40              45
192 Ser Thr Ala Ala Lys Leu Gly Leu Pro Pro Leu Thr Pro Glu Gln Gln
193              50              55              60
194 Glu Ala Leu Gln Lys Ala Lys Lys Tyr Ala Met Glu Gln Ser Ile Lys
195      65              70              75              80
196 Ser Val Leu Val Lys Gln Thr Ile Ala His Gln Gln Gln Gln Leu Thr
197              85              90              95
198 Asn Leu Gln Met Ala Ala Gln Arg Gln Arg Ala Leu Ala Ile Met Cys
199              100             105             110
200 Arg Val Tyr Val Gly Ser Ile Tyr Tyr Glu Leu Gly Glu Asp Thr Ile
201              115             120             125
202 Arg Gln Ala Phe Ala Pro Phe Gly Pro Ile Lys Ser Ile Asp Met Ser
203              130             135             140
204 Trp Asp Ser Val Thr Met Lys His Lys Gly Phe Ala Phe Val Glu Tyr
205      145             150             155             160
206 Glu Val Pro Glu Ala Ala Gln Leu Ala Leu Glu Gln Met Asn Ser Val
207              165             170             175
208 Met Leu Gly Gly Arg Asn Ile Lys Val Gly Arg Pro Ser Asn Ile Gly
209              180             185             190
210 Gln Ala Gln Pro Ile Ile Asp Gln Leu Ala Glu Glu Ala Arg Ala Phe
211              195             200             205
212 Asn Arg Ile Tyr Val Ala Ser Val His Gln Asp Leu Ser Asp Asp Asp
213              210             215             220
214 Ile Lys Ser Val Phe Glu Ala Phe Gly Lys Ile Lys Ser Cys Thr Leu
215      225             230             235             240
216 Ala Arg Asp Pro Thr Thr Gly Lys His Lys Gly Tyr Gly Phe Ile Glu
217              245             250             255
218 Tyr Glu Lys Ala Gln Ser Ser Gln Asp Ala Val Ser Ser Met Asn Leu
219              260             265             270
220 Phe Asp Leu Gly Gly Gln Tyr Leu Arg Val Gly Lys Ala Val Thr Pro
221              275             280             285
222 Pro Met Pro Leu Leu Thr Pro Ala Thr Pro Gly Glu Leu Pro Pro Ala
223              290             295             300
224 Ala Ala Val Ala Ala Ala Ala Thr Ala Lys Ile Thr Ala Gln Glu
225      305             310             315             320
226 Ala Val Ala Gly Ala Ala Val Leu Gly Thr Leu Gly Thr Pro Gly Leu
227              325             330             335
228 Val Ser Pro Ala Leu Thr Leu Ala Gln Pro Leu Gly Thr Leu Pro Gln
229              340             345             350
230 Ala Val Met Ala Ala Gln Ala Pro Gly Val Ile Thr Gly Val Thr Pro
231              355             360             365
232 Ala Arg Pro Pro Ile Pro Val Thr Ile Pro Ser Val Gly Val Val Asn
233              370             375             380
234 Pro Ile Leu Ala Ser Pro Pro Thr Leu Gly Leu Leu Glu Pro Lys Lys
235      385             390             395             400

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```

236 Glu Lys Glu Glu Glu Glu Leu Phe Pro Glu Ser Glu Arg Pro Glu Met
237                               405                               410                               415
238 Leu Ser Glu Gln Glu His Met Ser Ile Ser Gly Ser Ser Ala Arg His
239                               420                               425                               430
240 Met Val Met Gln Lys Leu Leu Arg Lys Gln Glu Ser Thr Val Met Val
241                               435                               440                               445
242 Leu Arg Asn Met Val Asp Pro Lys Asp Ile Asp Asp Asp Leu Glu Gly
243                               450                               455                               460
244 Glu Val Thr Glu Glu Cys Gly Lys Phe Gly Ala Val Asn Arg Val Ile
245 465                               470                               475                               480
246 Ile Tyr Gln Glu Lys Gln Gly Glu Glu Glu Asp Ala Glu Ile Ile Val
247                               485                               490                               495
248 Lys Ile Phe Val Glu Phe Ser Ile Ala Ser Glu Thr His Lys Ala Ile
249                               500                               505                               510
250 Gln Ala Leu Asn Gly Arg Trp Phe Ala Gly Arg Lys Val Val Ala Glu
251                               515                               520                               525
252 Val Tyr Asp Gln Glu Arg Phe Asp Asn Ser Asp Leu Ser Ala
253                               530                               535                               540

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255 &lt;210&gt; SEQ ID NO: 3

256 &lt;211&gt; LENGTH: 18

257 &lt;212&gt; TYPE: DNA

258 &lt;213&gt; ORGANISM: Artificial Sequence

260 &lt;220&gt; FEATURE:

261 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA

W--&gt; 262 &lt;400&gt; SEQUENCE: 3

263 ggcccatca agagcatg

18

265 &lt;210&gt; SEQ ID NO: 4

266 &lt;211&gt; LENGTH: 19

267 &lt;212&gt; TYPE: DNA

268 &lt;213&gt; ORGANISM: Artificial Sequence

270 &lt;220&gt; FEATURE:

271 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA

W--&gt; 272 &lt;400&gt; SEQUENCE: 4

273 ggggctgggc cagggtcag

19

275 &lt;210&gt; SEQ ID NO: 5

276 &lt;211&gt; LENGTH: 18

277 &lt;212&gt; TYPE: DNA

278 &lt;213&gt; ORGANISM: Artificial Sequence

280 &lt;220&gt; FEATURE:

281 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA

W--&gt; 282 &lt;400&gt; SEQUENCE: 5

283 gcacctggag tcatcaca

18

285 &lt;210&gt; SEQ ID NO: 6

286 &lt;211&gt; LENGTH: 19

287 &lt;212&gt; TYPE: DNA

288 &lt;213&gt; ORGANISM: Artificial Sequence

290 &lt;220&gt; FEATURE:

291 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA

293 &lt;400&gt; SEQUENCE: 6

## VERIFICATION SUMMARY

DATE: 11/01/2005

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TIME: 10:53:14

Input Set : A:\Q90951 Sequence Listing.txt

Output Set: N:\CRF4\11012005\J554026.raw

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L:5 M:283 W: Missing Blank Line separator, <130> field identifier  
L:6 M:270 C: Current Application Number differs, Replaced Current Application No  
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:8 M:283 W: Missing Blank Line separator, <160> field identifier  
L:262 M:283 W: Missing Blank Line separator, <400> field identifier  
L:272 M:283 W: Missing Blank Line separator, <400> field identifier  
L:282 M:283 W: Missing Blank Line separator, <400> field identifier